

## **AMENDMENTS TO THE CLAIMS**

This listing of claims will replace all prior versions and listings of claims in the application:

Claims 1-48 (Canceled).

49. (Currently Amended) ~~The polypeptide according to claim 27, wherein the viral genome is~~ A polypeptide fragment of a viral protein encoded by a nucleotide sequence from a viral genome selected from the group consisting of HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC and expressed by a method comprising:  
a) amplifying the nucleotide sequence encoding said polypeptide with at least two primers, wherein said first primer is complementary to a first region of nucleotides of a nucleic acid of said viral genome, and said second primer is complementary to a second region of nucleotides of a strand of DNA complementary to said nucleic acid of said viral genome, wherein said first and second regions of nucleotides are separated by about 100 to about 1100 base pairs, and said at least two primers are selected from the group of nucleotides, oriented in the 5' to 3' direction, consisting of:

SEQ ID NO:68;

nucleotides 6905-6930 (SEQ ID NO:46), 7055-7077 (SEQ ID NO:48), 7360-7384 (SEQ ID NO:49), 7832-7857 (SEQ ID NO:52), 8844-8869 (SEQ ID NO:53), 7629-7647 (SEQ ID NO:55), and 8224-8242 (SEQ ID NO:56) of the env gene of HIV-1 Bru;

nucleotides 6930-6905 (SEQ ID NO:47), 7384-7360 (SEQ ID NO:50), 7857-7832 (SEQ ID NO:51), 8869-8844 (SEQ ID NO:54), and nucleotides 8242-8224 (SEQ ID NO:57) of a nucleic acid sequence complementary to the *env* gene of HIV-1 Bru;

nucleotides 6903-6928 (SEQ ID NO:46), 7053-7075 (SEQ ID NO:48), 7349-7373 (SEQ ID NO:49), 7821-7846 (SEQ ID NO:52), 7612-7630 (SEQ ID NO:55), 8213-8231 (SEQ ID NO:56), and 8836-8861 (SEQ ID NO:53) of the *env* gene of HIV-1 Mal;

nucleotides 6928-6903 (SEQ ID NO:47), 7373-7349 (SEQ ID NO:50), 7846-7821 (SEQ ID NO:51), 8861-8836 (SEQ ID NO:54), and 8231-8213 (SEQ ID NO:57) of a nucleic acid sequence complementary to the *env* gene of HIV-1 Mal;

nucleotides 6860-6885 (SEQ ID NO:46), 7010-7032 (SEQ ID NO:48), 7306-7330 (SEQ ID NO:49), 7775-7800 (SEQ ID NO:52), 8787-8812 (SEQ ID NO:53), 7572-7590 (SEQ ID NO:55), and 8167-8185 (SEQ ID NO:56) of the *env* gene of HIV-1 Eli; and

nucleotides 6885-6860 (SEQ ID NO:47), 7330-7306 (SEQ ID NO:50), 7800-7775 (SEQ ID NO:51), 8812-8787 (SEQ ID NO:54), and 8185-8167 (SEQ ID NO:57) of a nucleic acid sequence complementary to the *env* gene of HIV-1 Eli;

b) introducing said amplified nucleotide sequence into a vector;

c) transforming a host cell with said vector;

d) placing said transformed host cell in culture; and

e) expressing said polypeptide.

50. (Currently Amended) ~~The polypeptide according to claim 28, wherein the viral genome is~~ A polypeptide fragment of a viral protein encoded by a nucleotide sequence from a viral genome selected from the group consisting of HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC and expressed by a method comprising:

a) amplifying the nucleotide sequence encoding said polypeptide with at least two primers, wherein said first primer is complementary to a first region of nucleotides of a nucleic acid of said viral genome, and said second primer is complementary to a second region of nucleotides of a strand of DNA complementary to said nucleic acid of said viral genome, wherein said first and second regions of nucleotides are separated by about 100 to about 1100 base pairs, and said at least two primers are selected from the group of nucleotides, oriented in the 5' to 3' direction, consisting of:

MMy5: CCA ATT CCC ATA CAT TAT TGT GCC CC (SEQ ID NO:46);

MMy5a: GGG GCA CAA TAA TGT ATG GGA ATT GG (SEQ ID NO:47);

MMy6: AAT GGC AGT CTA GCA GAA GAA GA (SEQ ID NO:48);

MMy7: ATC CTC AGG AGG GGA CCC AGA AAT T (SEQ ID NO:49);

MMy7a: AAT TTC TGG GTC CCC TCC TGA GGA T (SEQ ID NO:50);

MMy8: GTG CTT CCT GCT GCT CCC AAG AAC CC (SEQ ID NO:51);

MMy8a: GGG TTC TTG GGA GCA GCA GGA AGC AC (SEQ ID NO:52);

MMy9: ATG GGT GGC AAG TGG TCA AAA AGT AG (SEQ ID NO:53);

ATG GGT GGC AAA TGG TCA AAA AGT AG (SEQ ID NO:68);

MMy9a: CTA CTT TTT GAC CAC TTG CCA CCC AT (SEQ ID NO:54);

MMy78: TAT TAA CAA GAG ATG GTG G (SEQ ID NO:55);

MMy89: CCA GCA AGA AAA GAA TGA A (SEQ ID NO:56); and

MMy89a: TTC ATT CTT TTC TTG CTG G (SEQ ID NO:57);

b) introducing said amplified nucleotide sequence into a vector;

c) transforming a host cell with said vector;

d) placing said transformed host cell in culture; and

e) expressing said polypeptide.

51. (Currently Amended) The polypeptide according to claim 49 ~~38~~, wherein the viral genome is HIV-1 Bru, ~~HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.~~

52. (Currently Amended) The polypeptide according to claim 50 ~~39~~, wherein the viral genome is HIV-1 Bru, ~~HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.~~

53. (Currently Amended) The polypeptide according to claim 49, wherein the viral genome is ~~HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.~~

54. (Currently Amended) The polypeptide according to claim 50, wherein the viral genome is ~~HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.~~

55. (Currently Amended) The polypeptide according to claim 49 ~~54~~, wherein the viral genome is ~~HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.~~

56. (Currently Amended) The polypeptide according to claim 50 ~~52~~, wherein the viral genome is ~~HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.~~

57. (Currently Amended) The composition according to claim 49 ~~32~~, wherein the viral genome is ~~HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.~~

58. (Currently Amended) The composition according to claim 50 ~~33~~, wherein the viral genome is ~~HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.~~

59. (Currently Amended) The composition according to claim 49 ~~43~~, wherein the viral genome is ~~HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.~~

60. (Currently Amended) The composition according to claim 50 ~~claim 44~~, wherein the viral genome is ~~HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.~~

61. (Currently Amended) The composition according to claim 49 ~~57~~, wherein the composition further comprises a pharmaceutically acceptable vehicle ~~viral genome is HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.~~

62. (Currently Amended) The composition according to claim 50 ~~58~~, wherein the composition further comprises a pharmaceutically acceptable vehicle ~~viral genome is HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.~~

63-68. (Cancelled)